

Replacement Sheet 1 of 29

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FIG. 1

1 tgaggggccc atgaggagccc tgtgtgagc cccactctg ctctctctgc tgcgcgcgc
61 gctgtgtctc acgcccgcg ctgggaagc cgcctgctc accggggctt gtgacaagga
121 ctcccaatgt ggtgaggca tgtgctgtc tgtcagtac tgggtcaaga gcataaggat
181 ttgcacacct atgggcaaac tgggagacag ctgccatcca ctgactcgtg aaacaattt
241 tggaaatgga aggcaggaaa gaagaaagag gaagagaagc aaaaggaaaa aggaggttcc
301 atttttggg cggaggatgc atcacacttg cccatgtctg ccaggcttgg cotgtttaag
361 gacttcattt aaccgattta ttgttttagc ccaaaatgaa tgcgtctgga gtagaaccca
421 aatgtga

FIG. 2

MRSLCCAPLLLLLLLLLPFILLTPRAGDAAVITGACDKDSQCGGMC CAVSIWVKSIRICT
PMGKLGDSCHPLTRKNNFGNGRQERRKRKRKRKKEVPFFGGRMHHTCPCLPGLACLR
T
S
FNRFCICLAQK

FIG. 3

```
1   tgaggcgcc atgaggagcc tgtgtgcgc ccactctgc ctctcttg tgtagcgcc  
61  gagggcgcca tggaggagcct gtgtgcgc ccactctgc tctcttgt gtcgcgcgc  
121 ctgtgtgctca cgcgcgcgc tgggacgc gccgtgatca cggggcttg tgacaaggac  
181 tcccaatgtg gtggaggcat gtgtgtgt gtcagtatc gggtcaagag cataaggatt  
241 tgacacacta tgggcaact gggagacgc tccatccac tgactcgtaa agttccattt  
301 tttaggcgga ggaatgatca cactgcca tgtctgcag gcttgccg tttacggact  
361 tcatitaaac gatttatitg tttagccaa aagtaatcgc tctggagtag aaaccaaatg  
421 tga
```

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FIG. 4

MRSICCAPLLLLLLLLPPLLTFRAGDAVITGACDKDSQCGGMCACAVSIWKSIRICT
PMGKLIGDSCHPELTRKVPFFGRRMHTCPCLPGLACLRTSFNRFICLAQK

FIG. 5

1	cgagcgcgtg	ggcgctccct	aaccgccaac	gcgtcccccg	gacgccatgg	gggaccgcgcg
61	ctgtgcccg	ctactgcctac	ttctgtgct	accgctgctg	ttcacaccgc	cgcgcgggga
121	tgcgcggctc	atcacccggg	cttgcgacaa	ggactctcag	tgcggaggag	gcattgtctg
181	tgtgtcag	atctgggtta	agagcataag	gactgcaca	cctatggccc	aagtggcga
241	cagctgcac	ccctcgactc	ggaagtcc	atttgggg	cggaggatgc	accacactg
301	ccctgcctg	ccagcctgg	cgtgtttaag	gactctttc	aaccggitta	tttgcctggc
361	ccggaaaatg	tcactctgaa	ctagggaact	gaaatgcac	ccctcgtgc	acaatgccg
421	tcgagtctca	cttgaattg	tggcaacaa	agaatactc	agaaagaaat	gttctccccc
481	ttccttgact	ttccaagtaa	cgttctatc	tttgatttt	gaagtggctt	tttttttt
541	tttttttcc	tttctctgaa	ggaagtgtt	gattttgga	gagatttata	gaggactttc
601	tgacatggct	ttctattcc	ctgtttatg	tttgcctga	cattttgaa	tgcataaac
661	aactgttttc	acaaatagga	gaataagagg	gaacaatctg	ttgcgaaaac	ttccttttgc
721	actttgccc	actcgcctcg	cccgccccc	cccgccctg	cccatgcga	gacagacaca
781	cccttactct	tcaagactc	tgatgatct	caccttactg	tagcatttgg	ggtttctaca
841	cttcccgcct	ttgctgttgg	accactagag	gaggctcaga	gagctagcac	tgtacagggt
901	tgaaccagat	cccccaagca	gtctatttgg	ggcagacgtt	gggagcgtc	caggaacttt
961	cctgcaccca	tttgcccccac	tgcttttcag	ttctgtgtt	taactgttgg	gaggacaaaa
1021	ttaacgggac	cttgaaggaa	cctgccctg	ttctctagat	ttgtttaagt	aaagacatt
1081	ttctccttgt	tgtggaatat	tacatgctt	tttctttttt	atctgaagct	ttttttttt
1141	ttctttaagt	cttctgttgg	gagacatttt	aaagaacgc	actcagaggaa	gcattgattt
1201	tcarytgcca	tgacaggagt	catcatttta	aaaaatcggt	gttaagttat	aatttaaac
1261	ttattgttaa	cccaagggtg	taatgtaaat	ggatttctctg	atatctgccc	atttgtactg
1321	gtatcaatat	tttataatg				

FIG. 6

MGDPRCAPLLLLLLLLLPLLLFTPPAGDAAVITGACDKDSQC GGMCCAVSIWVKSIRICTP
MGQVGDSCHPLTRKVPFWGRRMHHTCPCLPGLACLR T SFNRFI CLARK

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Fig. 7

FIG. 8

1 tggctccccc agcttgccag gcacaaggct gagcgggagg aagcgagagg catctaagca ggcagtgttt
 71 tgctctacc ccaagtgaac atgagaggtg ccacgaggt ctaatcatg ctctctctag taactgtgtc
 141 tgaatgtgtc gtatcacag gggcctgtga ggggatgtc cagtgtggg caggcaactg ctgtgccatc
 211 agcctgtggc ttcgaggct ggggatgtgc acccgcgtg ggcgggaagg cgaggagtgc caccocggca
 281 gcacaagggt ccccttcttc aggaacgca agcacacac ctgtccttg ttgcccaacc tgctgtgtc
 351 caggttcccg gagggcagg accgtgtctc catgacttg aagaatcga attttaggc gcttgctctg
 421 tctcaggata ccacacatcc ttctctgag cacagcctgg attttatit ctgccatgaa acccagctcc
 491 catgactctc ccagtcccta cactgactac cctgatctct ctgtctagt acgcacatat gcacacggc
 561 agacataact cccatcatga catgttcccc aggtggcct gagatgtca cagettgagg ctgtgtgtg
 631 aaagtggtgc agctgtgtc tcttctctgc tcaggctgcc agagagtggt taatggcag aaaggacatt
 701 cccctccccc tcccagggt accgtgtctc ttctctgggc cctgcacctc tcccacatg tatccctgg
 771 tctgaattag acattcttg gcacaggctc ttgggtgcat tgctcagagt cccaggtcct ggcctgaacc
 841 tcaggccctt cagtgagggt ctgtgaggac caattgtgg gtatgtcat ttccctogat tggttaactc
 911 cttagtttca gaccacagac tcaagattgg cctttccag agggcagcag acagtcaacc caagcgagt
 981 gtaggagacc cagggagacc aatcagcccc ctgaagactc tggtcccagt cagctgtgg ctgtgtgct
 1051 gtgacctgtg acctctgac agaatgtca tgctctgag gccctctctt accacacttt accagttaac
 1121 cactgaagcc cccaattccc acagcttttc cattaaatg caaatgttg tggttcaatc taatctgata
 1191 ttgacatatt agaaggcaat taggtgtttt ccttaacaaa ctctttcca aggatcagcc ctgagagcag
 1261 gtgtgtgact ttgaggagg cagtctctg tccagatgg ggtgggagca agggacaggg agcagggcag
 1331 gggctgaaag gggcactgat tcagaccagg gaggcaacta cacaccaaca tgcgtgcttt agaataaaag
 1401 caccactgta aaaaa

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1   GAA GTG AGG GGT ACC AAA GTA GAC TGT GTT TGT CGT CAC CTC AAG TGA TC

51  ATG AGA GGC GCT GTG CAT ATC TTC ATG CTC CTT CTA GCA ACG GCG TCC
    M R G A V H I F I M L L A T A S

102 GAC TGT GCG GTC ATC ACA GGG GGC TGT GAA CGA GAT ATC CAG TGT GGG GGC
    D C A V I T G A C E R D I Q C G A

153 GGC ACC TGC TGC GCT ATC AGT CTG TGG CTG GGG GGC CTG CGG TTG TGT ACC
    G T C C A I S L W L R G L R L C T

204 CCA CTG GGG CGT GAA GGA GAG GAG TGC CAC CCA GGA AGC CAC AAG ATC CCC
    P L G R E G E E C H P G S H K I P

255 TTC TTG AGG AAA CGC CAA CAC CAT ACC TGT CCC TGC TCA CCC AGC CTG CTG
    F L R K R Q H H T C P C S P S L L

306 TGC TCC AGG TTC CCG GAC GGC AGG TAC CGC TGC TTC CGG GAC TTG AAG AAT
    C S R F P D G R Y R C F R D L K N

357 GCC AAC TTT TAGTTGTCTGGACTCTGTCTGGAGCCTGACTGGGTGACCTCTTGCTTACACCT
    A N F *

    GTGTGATTTAGCTCCCTGCAACTTCGCCATTCCCATCTTTCGGTGTATGTGCAGACAGGAGACC
    TTCGCGTATGGAATAGTTCCACAGGTGACAGAGGAGTTCGTGSCCTTGAGAGTTGGCCAGCCCG
    ACCTTCGTCGCTCAGACTGCGCTGAAGTTGTGACAGTGTGGGCCCTTCTCAGTTGCCTGCCCTTCCG
    CATGTGCGCTTCTTCTAAACACACACCTTTCTGGCACTGGCCATGGATGCACCACTAAATCAACA
    GGTCTGTGGGTGGATGATCAACTTCTCTCCATTTTCTTTTATTGACTGGCTTCTCTAATTTAAGG
    ACTGT

```

FIG. 10

FIG. 11

	10	20	30	40	50	
human	EG-VEGF	MRGATRVSIM	LLLVTVSDCA	VITGACERDV	QCGAGTCCAI	SLWLRGLRMC
murine	EG-VEGF	MRGAVHIFIM	LLLATASDCA	VITGACERDI	QCGAGTCCAI	SLWLRGLRLC
	60	70	80	90	100	105
human	EG-VEGF	TPLGREGEEC	HPGSHKVPEFF	RKRKHHTCP	LPNLLCSRFP	DGRYRCMDL KNINF
murine	EG-VEGF	TPLGREGEEC	HPGSHKIEFL	RKRQHHTCP	SPSLLCSRFP	DGRYRCERDL KNANF

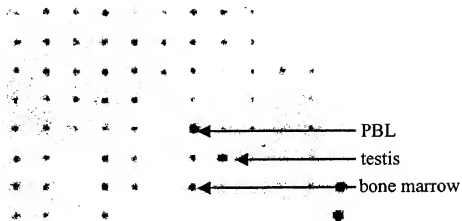
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FIG. 12

Human BV8	28	AVITGACDKDSQCGGMCCAVSIWKSIRICTPMGKLGDSCHPLTRKVPF
	20	
Human EG-VEGF		AVITGACERDVQCGAGTCCCAISLWRLGLRMCTPLGREGECHPGSHKVPF
	78	108
Human BV8		FGRRMHHTCPCLPGLACLRTSFNRFICLAQK
	70	105
Human EG-VEGF		FRKKHHTCPCLPNLLCSRFPPDGRYRCSMDLKNIF

FIG. 13



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FIG. 14A

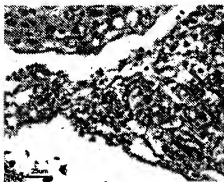


FIG. 14B

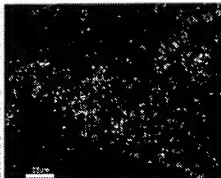


FIG. 14C

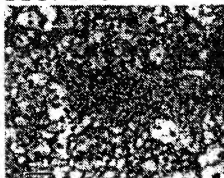
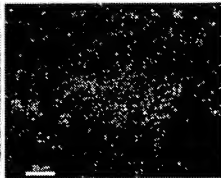


FIG. 14D



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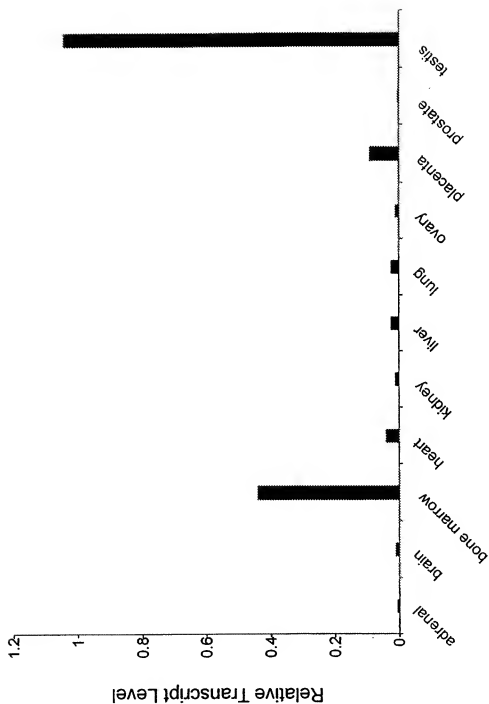


FIG. 15A

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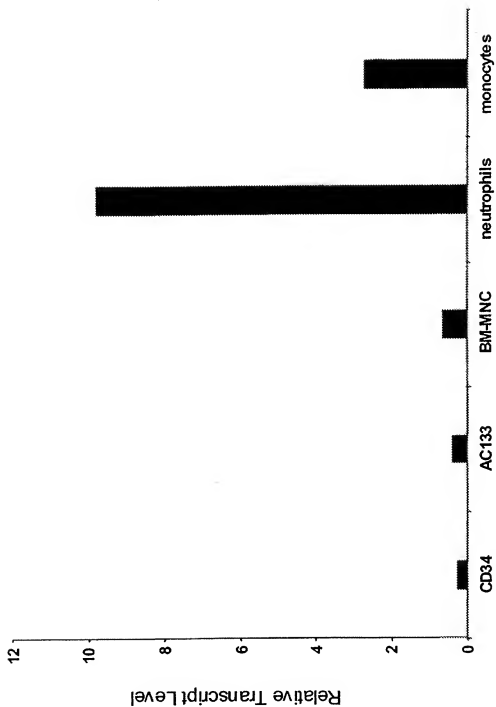
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FIG. 15B



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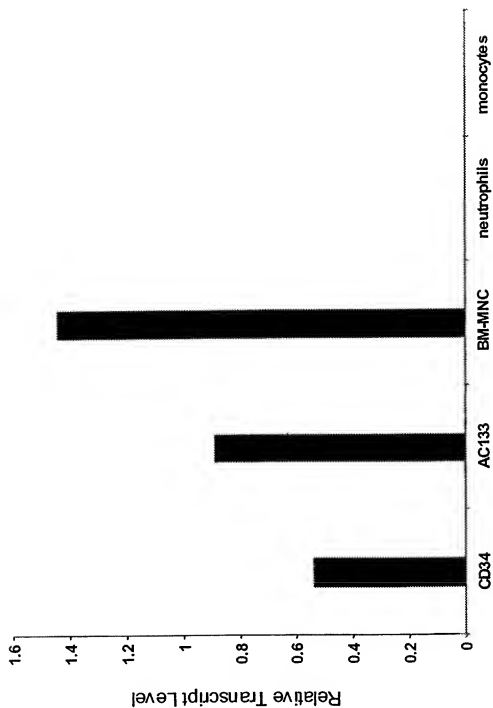
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FIG. 15C



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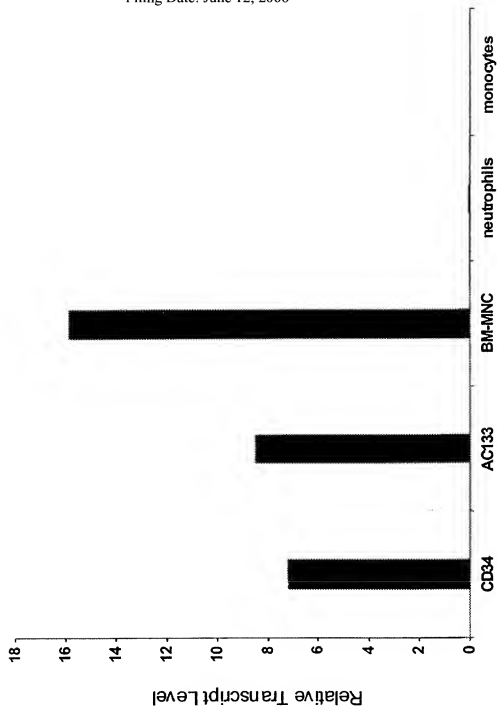
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FIG. 15D



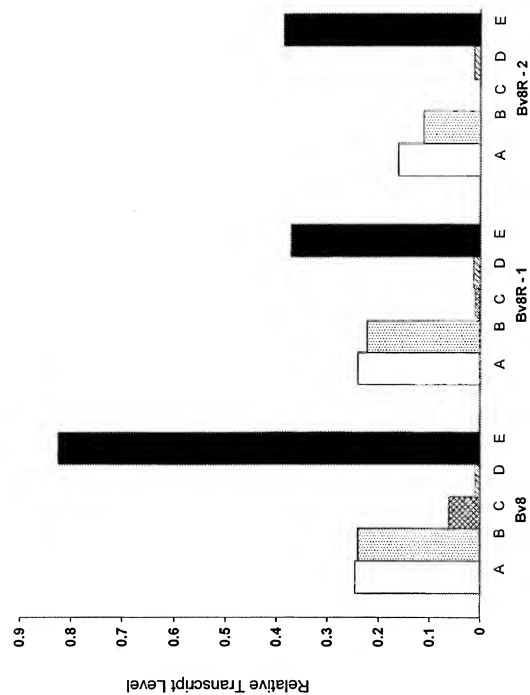
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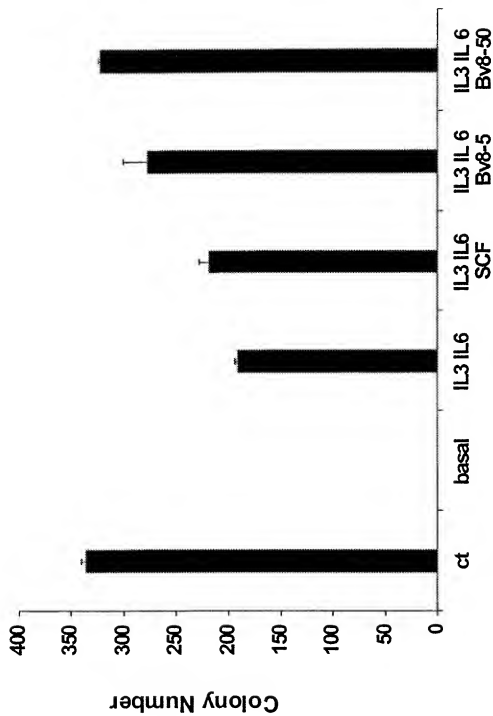
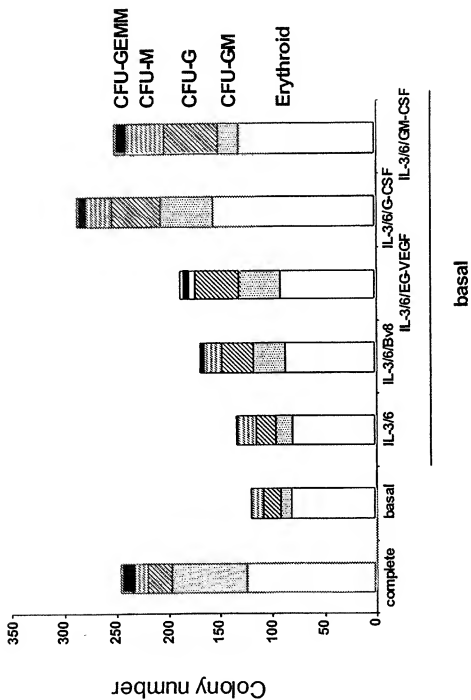
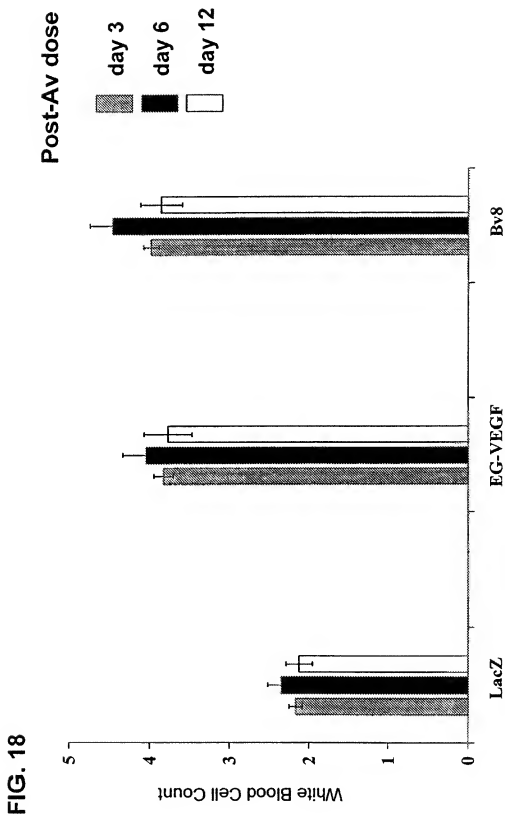
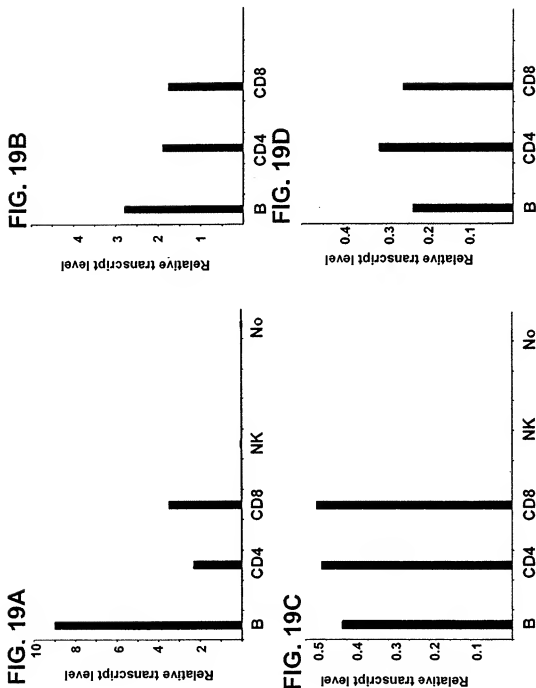


FIG. 17A

FIG. 17B







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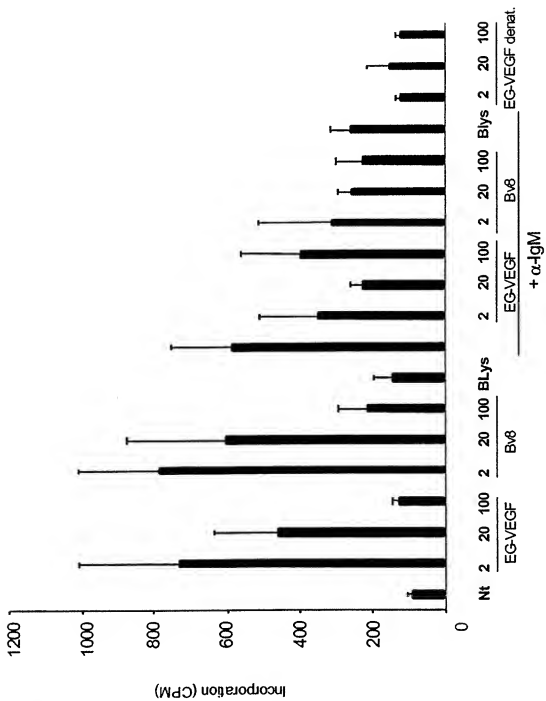


FIG. 20

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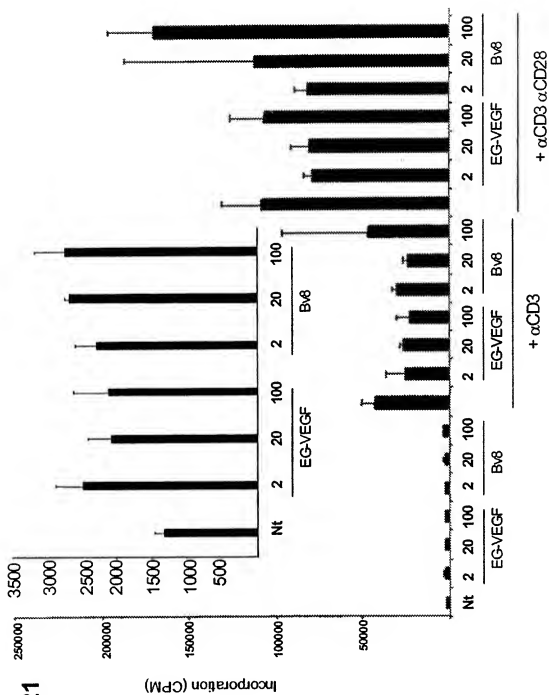




FIG. 22A

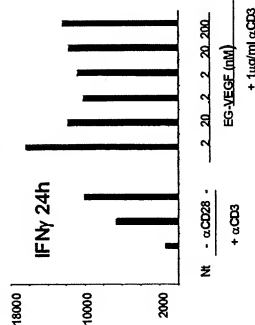


FIG. 22C

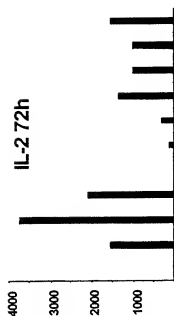


FIG. 22B

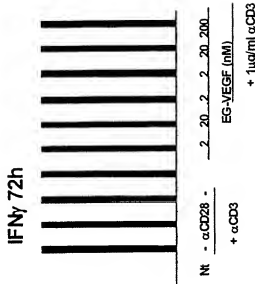


FIG. 22D

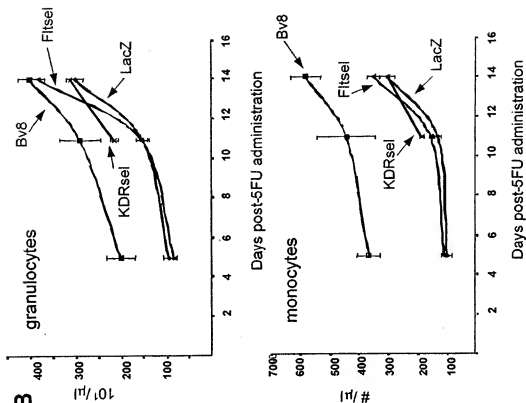


FIG. 23C

FIG. 23B

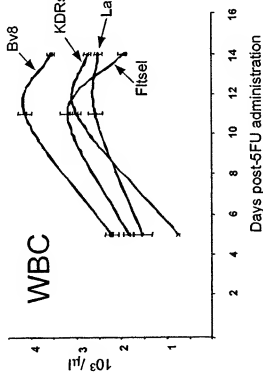


FIG. 23A

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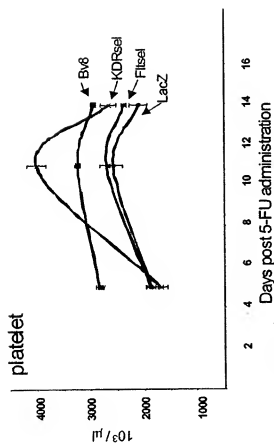


FIG. 23D

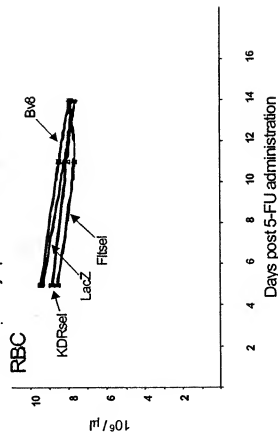


FIG. 23E

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FIG. 24

